

PCT

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/744,016

DATE: 05/23/2001  
TIME: 12:31:17

Input Set : A:\PTO.txt  
Output Set: C:\CRF3\05232001\I744016.raw

Does Not Comply  
Corrected Diskette Needed

W--> 1 SEQUENZPROTOKOLL *delete this*  
3 <110> APPLICANT: Dr. Volkel, Helge  
5 <120> TITLE OF INVENTION: Method for screening of modulators of calcineurin  
6 activity  
8 <130> FILE REFERENCE: A34157PCT  
10 <140> CURRENT APPLICATION NUMBER: US/09/744,016  
11 <141> CURRENT FILING DATE: 2001-05-07  
13 <150> PRIOR APPLICATION NUMBER: EP98113876  
14 <151> PRIOR FILING DATE: 1998-07-22  
16 <160> NUMBER OF SEQ ID NOS: 35  
18 <170> SOFTWARE: PatentIn Ver. 2.1

## ERRORED SEQUENCES

2767 <210> SEQ ID NO: 20  
2768 <211> LENGTH: 5525  
2769 <212> TYPE: DNA  
2770 <213> ORGANISM: Homo sapiens  
2772 <220> FEATURE:  
2773 <221> NAME/KEY: CDS  
2774 <222> LOCATION: (115)..(1686)  
2775 <223> OTHER INFORMATION: histidine tagged calcineurin A alpha2  
2777 <220> FEATURE:  
2778 <221> NAME/KEY: misc\_feature  
2779 <222> LOCATION: (1687)..(1728)  
2780 <223> OTHER INFORMATION: ribosomal binding site, multiple cloning site 2  
2782 <220> FEATURE:  
2783 <221> NAME/KEY: CDS  
2784 <222> LOCATION: (1729)..(2241)  
2785 <223> OTHER INFORMATION: calcineurin B  
2787 <400> SEQUENCE: 20  
2788 ctcgagaaat cataaaaaat ttatttgctt tgtgagcgga taacaattat aatagattca 60  
2790 attgtgagcg gataacaatt tcacacagaa ttcattaaag aggagaaatt aact atg 117  
2791 Met  
2792 1  
2794 aga gga tcg cat cac cat cac cat cac gga tcc atg tcc gag ccc aag 165  
2795 Arg Gly Ser His His His His His His Gly Ser Met Ser Glu Pro Lys  
2796 5 10 15  
2798 gca att gat ccc aag ttg tcg acg acc gac agg gtg gtg aaa gct gtt 213  
2799 Ala Ile Asp Pro Lys Leu Ser Thr Thr Asp Arg Val Val Lys Ala Val  
2800 20 25 30  
2802 cca ttt cct cca agt cac cgg ctt aca gca aaa gaa gtg ttt gat aat 261  
2803 Pro Phe Pro Pro Ser His Arg Leu Thr Ala Lys Glu Val Phe Asp Asn  
2804 35 40 45  
2806 gat gga aaa cct cgt gtg gat atc tta aag gcg cat ctt atg aag gag 309  
2807 Asp Gly Lys Pro Arg Val Asp Ile Leu Lys Ala His Leu Met Lys Glu

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2808	50	55	60	65	357
2810	gga agg ctg gaa gag agt gtt gca ttg aga ata ata aca gag ggt gca				
2811	Gly Arg Leu Glu Glu Ser Val Ala Leu Arg Ile Ile Thr Glu Gly Ala				
2812	70	75	80		
2814	tca att ctt cga cag gaa aaa aat ttg ctg gat att gat gcg cca gtc				405
2815	Ser Ile Leu Arg Gln Glu Lys Asn Leu Leu Asp Ile Asp Ala Pro Val				
2816	85	90	95		
2818	act gtt tgt ggg gac att cat gga caa ttc ttt gat ttg atg aag ctc				453
2819	Thr Val Cys Gly Asp Ile His Gly Gln Phe Phe Asp Leu Met Lys Leu				
2820	100	105	110		
2822	ttt gaa gtc ggg gga tct cct gcc aac act cgc tac ctc ttc tta ggg				501
2823	Phe Glu Val Gly Gly Ser Pro Ala Asn Thr Arg Tyr Leu Phe Leu Gly				
2824	115	120	125		
2826	gac tat gtt gac aga ggg tac ttc agt att gaa tgt gtg ctg tat ttg				549
2827	Asp Tyr Val Asp Arg Gly Tyr Phe Ser Ile Glu Cys Val Leu Tyr Leu				
2828	130	135	140		
2830	tgg gcc ttg aaa att ctc tac ccc aaa aca ctg ttt tta ctt cgt gga				597
2831	Trp Ala Leu Lys Ile Leu Tyr Pro Lys Thr Leu Phe Leu Leu Arg Gly				
2832	150	155	160		
2834	aat cat gaa tgt aga cat cta aca gag tat ttc aca ttt aaa caa gaa				645
2835	Asn His Glu Cys Arg His Leu Thr Glu Tyr Phe Thr Phe Lys Gln Glu				
2836	165	170	175		
2838	tgt aaa ata aag tat tca gaa cga gta tat gat gcc tgt atg gat gcc				693
2839	Cys Lys Ile Lys Tyr Ser Glu Arg Val Tyr Asp Ala Cys Met Asp Ala				
2840	180	185	190		
2842	ttt gac tgc ctt ccc ctg gct gcc ctg atg aac caa cag ttc ctg tgt				741
2843	Phe Asp Cys Leu Pro Leu Ala Ala Leu Met Asn Gln Gln Phe Leu Cys				
2844	195	200	205		
2846	gtg cat ggt ggt ttg tct cca gag att aac act tta gat gat atc aga				789
2847	Val His Gly Gly Leu Ser Pro Glu Ile Asn Thr Leu Asp Asp Ile Arg				
2848	210	215	220		
2850	aaa tta gac cga ttc aaa gaa cca cct gca tat gga cct atg tgt gat				837
2851	Lys Leu Asp Arg Phe Lys Glu Pro Pro Ala Tyr Gly Pro Met Cys Asp				
2852	230	235	240		
2854	atc ctg tgg tca gac ccc ctg gaa gat ttt gga aat gag aag act cag				885
2855	Ile Leu Trp Ser Asp Pro Leu Glu Asp Phe Gly Asn Glu Lys Thr Gln				
2856	245	250	255		
2858	gaa cat ttc act cac aac aca gtc agg ggg tgt tca tac ttc tac agt				933
2859	Glu His Phe Thr His Asn Thr Val Arg Gly Cys Ser Tyr Phe Tyr Ser				
2860	260	265	270		
2862	tac ccg gct gta tgt gaa ttc tta cag cac aat aac ttg tta tct ata				981
2863	Tyr Pro Ala Val Cys Glu Phe Leu Gln His Asn Asn Leu Leu Ser Ile				
2864	275	280	285		
2866	ctc cga gcc cac gaa gcc caa gat gca ggg tac cgc atg tac agg aaa				1029
2867	Leu Arg Ala His Glu Ala Gln Asp Ala Gly Tyr Arg Met Tyr Arg Lys				
2868	290	295	300		
2870	agc caa aca aca ggc ttc cct tct cta att aca att ttt tca gca cca				1077
2871	Ser Gln Thr Thr Gly Phe Pro Ser Leu Ile Thr Ile Phe Ser Ala Pro				
2872	310	315	320		

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Input Set : A:\PTO.txt  
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2874 aat tac tta gat gta tac aat aac aaa gct gca gta ttg aag tat gag 1125  
2875 Asn Tyr Leu Asp Val Tyr Asn Asn Lys Ala Ala Val Leu Lys Tyr Glu 335  
2876 325 330  
2878 aac aat gtt atg aat atc agg caa ttc aac tgt tct cct cat cca tac 1173  
2879 Asn Asn Val Met Asn Ile Arg Gln Phe Asn Cys Ser Pro His Pro Tyr 350  
2880 340 345  
2882 tgg ctt cca aat ttc atg gat gtt ttt act tgg tcc ctt cca ttt gtt 1221  
2883 Trp Leu Pro Asn Phe Met Asp Val Phe Thr Trp Ser Leu Pro Phe Val 365  
2884 355 360  
2886 ggg gaa aaa gtg act gag atg ctg gta aat gtc ctc aac atc tgc tca 1269  
2887 Gly Glu Lys Val Thr Glu Met Leu Val Asn Val Leu Asn Ile Cys Ser 385  
2888 370 375  
2890 gat gat gaa cta ggg tca gaa gaa gat gga ttt gat ggt gca aca gct 1317  
2891 Asp Asp Glu Leu Gly Ser Glu Glu Asp Gly Phe Asp Gly Ala Thr Ala 400  
2892 390 395  
2894 gca gcc cgg aaa gag gtg ata agg aac aag atc cga gca ata ggc aaa 1365  
2895 Ala Ala Arg Lys Glu Val Ile Arg Asn Lys Ile Arg Ala Ile Gly Lys 415  
2896 405 410  
2898 atg gcc aga gtg ttc tca gtg ctc aga gaa gag agt gag agt gtg ctg 1413  
2899 Met Ala Arg Val Phe Ser Val Leu Arg Glu Glu Ser Glu Ser Val Leu 430  
2900 420 425  
2902 acg ctg aaa ggc ttg acc cca act ggc atg ctc ccc agc gga gta ctt 1461  
2903 Thr Leu Lys Gly Leu Thr Pro Thr Gly Met Leu Pro Ser Gly Val Leu 445  
2904 435 440  
2906 tct gga ggg aag caa acc ctg caa agc gct atc aaa gga ttt tca cca 1509  
2907 Ser Gly Gly Lys Gln Thr Leu Gln Ser Ala Ile Lys Gly Phe Ser Pro 465  
2908 450 455  
2910 caa cat aag atc act agc ttc gag gaa gcc aag ggc tta gac cga att 1557  
2911 Gln His Lys Ile Thr Ser Phe Glu Glu Ala Lys Gly Leu Asp Arg Ile 480  
2912 470 475  
2914 aat gag agg atg ccg cct cgc aga gat gcc atg ccc tct gac gcc aac 1605  
2915 Asn Glu Arg Met Pro Pro Arg Arg Asp Ala Met Pro Ser Asp Ala Asn 495  
2916 485 490  
2918 ctt aac tcc atc aac aag gct ctc acc tca gag act aac ggc acg gac 1653  
2919 Leu Asn Ser Ile Asn Lys Ala Leu Thr Ser Glu Thr Asn Gly Thr Asp 510  
2920 500 505  
2922 agc aat ggc agt aat agc agc aat att cag tga ttaactaggg taccocgggg 1706  
2923 Ser Asn Gly Ser Asn Ser Ser Asn Ile Gln 520  
2924 515 520  
2926 taccaaagag gagaaattaa ct atg gga aat gag gca agt tat cct ttg gaa 1758  
2927 Met Gly Asn Glu Ala Ser Tyr Pro Leu Glu 530  
W--> 2928 525 530  
2930 atg tgc tca cac ttt gat gca gat gaa att aaa agg cta gga aag aga 1806  
2931 Met Cys Ser His Phe Asp Ala Asp Glu Ile Lys Arg Leu Gly Lys Arg 545 550  
W--> 2932 535 540 545  
2934 ttt aag aag ctc gat ttg gac aat tct ggt tct ttg agt gtg gaa gag 1854  
2935 Phe Lys Lys Leu Asp Leu Asp Asn Ser Gly Ser Leu Ser Val Glu Glu 560 565  
W--> 2936 555 560  
2938 ttc atg tct cta cct gag tta caa cag aat ccc tta gta cag cga gta 1902

5/23/01

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2939 Phe Met Ser Leu Pro Glu Leu Gln Gln Asn Pro Leu Val Gln Arg Val
W--> 2940          570          575          580          1950
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2943 Ile Asp Ile Phe Asp Thr Asp Gly Asn Gly Glu Val Asp Phe Lys Glu
W--> 2944          585          590          595          1998
2946 ttc att gag gga gtc tct cag ttc agt gtc aaa gga gat aag gaa cag
2947 Phe Ile Glu Gly Val Ser Gln Phe Ser Val Lys Gly Asp Lys Glu Gln
W--> 2948          600          605          610          2046
2950 aag ttg agg ttt gct ttc cgt atc tat gac atg gat aaa gac ggc tat
2951 Lys Leu Arg Phe Ala Phe Arg Ile Tyr Asp Met Asp Lys Asp Gly Tyr
W--> 2952 615          620          625          630          2094
2954 att tcc aat ggg gaa ctc ttc cag gtg cta aag atg atg gtg ggg aac
2955 Ile Ser Asn Gly Glu Leu Phe Gln Val Leu Lys Met Met Val Gly Asn
W--> 2956          635          640          645          2142
2958 aat ctg aaa gat aca cag tta cag caa att gta gac aaa acc ata ata
2959 Asn Leu Lys Asp Thr Gln Leu Gln Gln Ile Val Asp Lys Thr Ile Ile
W--> 2960          650          655          660          2190
2962 aat gca gat aag gat ggg gat gga aga ata tcc ttt gaa gaa ttc tgt
2963 Asn Ala Asp Lys Asp Gly Asp Gly Arg Ile Ser Phe Glu Glu Phe Cys
W--> 2964          665          670          675          2238
2966 gct gtt gta ggc ggc cta gat atc cac aaa aag atg gtg gta gat gtg
2967 Ala Val Val Gly Gly Leu Asp Ile His Lys Lys Met Val Val Asp Val
W--> 2968          680          685          690          2291
2970 tga ttaattagaa gcttaattag ctgagcttgg actcctgttg atagatccag
E--> 2972 695 delete
2974 taatgacctc agaactccat ctggatttgt tcagaacgct cggttgccgc cgggcgtttt 2351
2976 ttattggtga gaatccaagc tagcttggcg agattttcag gagctaagga agctaaaatg 2411
2978 gagaaaaaaa tcaactggata taccaccgtt gatatatccc aatggcatcg taaagaacat 2471
2980 tttgaggcat ttcagtcagt tgctcaatgt acctataacc agaccgttca gctggatatt 2531
2982 acggcctttt taaagaccgt aaagaaaaat aagcacaagt tttatccggc ctttattcac 2591
2984 attcttgccc gctgatgaa tgctcatccg gaatttcgta tggcaatgaa agacggtgag 2651
2986 ctggtgatata gggatagtgt tcacccttgt tacaccgttt tccatgagca aactgaaacg 2711
2988 ttttcatcgc tctggagtga ataccacgac gatttccggc agtttctaca catatattcg 2771
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2994 aatatggaca acttcttcgc ccccgttttc accatgggca aatattatac gcaaggcgac 2951
2996 aaggtgctga tgccgctggc gattcaggtt catcatgccg tctgtgatgg cttccatgtc 3011
2998 ggcagaatgc ttaatgaatt acaacagtac tgcatgagat ggcagggcgg ggcgtaattt 3071
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3016 tccgtctgtc ggctgcggcg agcggtatca gctcactcaa aggcggtaat acggttatcc 3611
3018 acagaatcag gggataacgc aggaaagaac atgtgagcaa aaggccagca aaaggccagg 3671
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3022 cacaaaaaatc gacgctcaag tcagaggtgg cgaaacccga caggactata aagataaccag 3791
3024 gcgttttcccc ctggaagctc cctcgtgcgc tctcctgttc cgaccctgcc gcttaccgga 3851
3026 tacctgtccg cttttctccc ttogggaagc gtggcgcttt ctcaatgctc acgctgtagg 3911
3028 tatctcagtt cgggttaggt cggtcgctcc aagctgggct gtgtgcacga acccccgtt 3971
3030 cagcccgacc gctgcgcctt atccggtaac tatcgtcttg agtccaaccc ggtaagacac 4031
3032 gacttatcgc cactggcagc agccactggt aacaggatta gcagagcgag gtatgtaggc 4091
3034 ggtgctacag agttcttgaa gtggtggcct aactacggct acactagaag gacagtattt 4151
3036 ggtatctgcg ctctgctgaa gccagttacc ttcggaaaaa gagttggtag ctcttgatcc 4211
3038 ggcaaacaaa ccaccgctgg tagcgggtgg ttttttggtt gcaagcagca gattacgcgc 4271
3040 agaaaaaaag gatctcaaga agatcctttg atcttttcta cggggtctga cgctcagtgg 4331
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3044 atccttttaa attaaaaatg aagttttaaa tcaactataa gtatatatga gtaaacttgg 4451
3046 tctgacagtt accaatgctt aatcagtgag gcacctatct cagcgatctg tctatttcgt 4511
3048 tcatccatag ctgectgact ccccgctcgt tagataacta cgatacggga gggcttacca 4571
3050 tctggcccca gtgctgcaat gataccgcga gaccacgct caccggctcc agatttatca 4631
3052 gcaataaacc agccagccgg aagggccgag cgcagaagtg gtctgcaac tttatccgcc 4691
3054 tccatccagt ctattaattg ttgcccggaa gctagagtaa gtagttcgcc agttaatagt 4751
3056 ttgcgcaacg ttgttgccat tgctacaggc atcgtggtgt cagcgtcgct gtttggtatg 4811
3058 gcttcattca gctccggttc ccaacgatca aggcgagtta catgatcccc catgttgtgc 4871
3060 aaaaaagcgg ttagtccctt cggctcctcg atcgttgtca gaagtaagtt ggccgcagtg 4931
3062 ttatcactca tggttatggc agcactgcat aattctctta ctgtcatgcc atccgtaaga 4991
3064 tgcttttctg tgactgtgta gtactcaacc aagtcattct gagaatagtg tatgcccga 5051
3066 ccgagttgct cttgcccgcc gtcaatacgg gataataccg cgccacatag cagaacttta 5111
3068 aaagtgtca tcattgaaa acgttcttcg gggcgaaaac tctcaaggat cttaccgctg 5171
3070 ttgagatcca gttcgatgta acccactcgt gcacccaact gatcttcagc atcttttact 5231
3072 ttcaccagcg tttctgggtg agcaaaaaca ggaaggcaaa atgccgcaaa aaagggaata 5291
3074 agggcgacac ggaaatggtg aatactcata ctcttccttt ttcaatatta ttgaagcatt 5351
3076 tatcagggtt attgtctcat gagcggatac atatttgaat gtatttagaa aaataaacia 5411
3078 ataggggttc cgcgcacatt tccccgaaaa gtgccacctg acgtctaaga aaccattatt 5471
3080 atcatgacat taacctataa aaataggcgt atcacgaggc cctttcgtct tcac 5525

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3657 <210> SEQ ID NO: 25

3658 <211> LENGTH: 170

3659 <212> TYPE: PRT

3660 <213> ORGANISM: Homo sapiens

3662 <400> SEQUENCE: 25

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3664 1 5 10 15

E--> 3666 Xaa Asp Glu Ile Lys Arg Leu Gly Lys Arg Phe Lys Lys Xaa Asp Leu  
3667 20 25 30

E--> 3669 Asp Asn Ser Gly Ser Leu Ser Val Glu Glu Phe Met Ser Xaa Pro Glu  
3670 35 40 45

E--> 3672 Leu Gln Gln Asn Xaa Leu Val Gln Arg Val Ile Asp Ile Phe Asp Thr  
3673 50 55 60

E--> 3675 Asp Gly Asn Gly Glu Val Asp Phe Lys Glu Phe Ile Glu Xaa Val Ser  
3676 65 70 75 80

3678 Gln Phe Ser Val Lys Gly Asp Lys Glu Gln Lys Leu Arg Phe Ala Phe  
3679 85 90 95

3681 Arg Ile Tyr Asp Met Asp Lys Asp Gly Tyr Ile Ser Asn Gly Glu Leu  
3682 100 105 110

*see  
item 10  
on Enon  
summary  
sheet*

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E--> 3684 Phe Gln Xaa Xaa Lys Met Met Val Gly Asn Asn Leu Lys Asp Thr Gln  
3685 115 120 125

E--> 3687 Leu Gln Gln Ile Val Asp Lys Thr Ile Ile Asn Ala Asp Lys Asp Xaa  
3688 130 135 140

E--> 3690 Asp Gly Arg Ile Ser Phe Glu Glu Phe Cys Ala Val Val Xaa Gly Leu  
3691 145 150 155 160

3693 Asp Ile His Lys Lys Met Val Val Asp Val  
3694 165 170

4132 <210> SEQ ID NO: 28  
4133 <211> LENGTH: 170  
4134 <212> TYPE: PRT  
4135 <213> ORGANISM: Homo sapiens  
4137 <400> SEQUENCE: 28

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4139 1 5 10 15

E--> 4141 Xaa Asp Glu Ile Lys Arg Leu Gly Lys Arg Phe Lys Lys Xaa Asp Leu  
4142 20 25 30

E--> 4144 Asp Asn Ser Gly Ser Leu Ser Val Glu Glu Phe Met Ser Xaa Pro Glu  
4145 35 40 45

E--> 4147 Leu Gln Gln Asn Xaa Leu Val Gln Arg Val Ile Asp Ile Phe Asp Thr  
4148 50 55 60

E--> 4150 Asp Gly Asn Gly Glu Val Asp Phe Lys Glu Phe Ile Glu Xaa Val Ser  
4151 65 70 75 80

4153 Gln Phe Ser Val Lys Gly Asp Lys Glu Gln Lys Leu Arg Phe Ala Phe  
4154 85 90 95

4156 Arg Ile Tyr Asp Met Asp Lys Asp Gly Tyr Ile Ser Asn Gly Glu Leu  
4157 100 105 110

E--> 4159 Phe Gln Xaa Xaa Lys Met Met Val Gly Asn Asn Leu Lys Asp Thr Gln  
4160 115 120 125

E--> 4162 Leu Gln Gln Ile Val Asp Lys Thr Ile Ile Asn Ala Asp Lys Asp Xaa  
4163 130 135 140

E--> 4165 Asp Gly Arg Ile Ser Phe Glu Glu Phe Cys Ala Val Val Xaa Gly Leu  
4166 145 150 155 160

4168 Asp Ile His Lys Lys Met Val Val Asp Val  
4169 165 170

5106 <210> SEQ ID NO: 35  
5107 <211> LENGTH: 19  
5108 <212> TYPE: PRT  
5109 <213> ORGANISM: Bos taurus  
5111 <220> FEATURE:  
5112 <221> NAME/KEY: PEPTIDE  
5113 <222> LOCATION: (1)..(19)  
5114 <223> OTHER INFORMATION: peptide of cAMP regulated protein kinase A, RII  
5116 <220> FEATURE:  
5117 <221> NAME/KEY: MOD\_RES  
5118 <222> LOCATION: (15)  
5119 <223> OTHER INFORMATION: PHOSPHORYLATION  
5121 <220> FEATURE:  
5122 <221> NAME/KEY: SITE

*Item 10*

*Item 10*

*Item 10*

*P.7*

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/744,016

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TIME: 12:31:18

Input Set : A:\PTO.txt  
Output Set: C:\CRF3\05232001\I744016.raw

5123 <222> LOCATION: (15)  
5124 <223> OTHER INFORMATION: artificial chemical modification by  
5125       fluorescein-phosphoramidite  
5127 <400> SEQUENCE: 35  
5128 Asp Leu Asp Val Pro Ile Pro Gly Arg Phe Asp Arg Arg Val Ser Val  
5129    1                               5                               10                               15  
5131 Ala Ala Glu

E--> 5136 A 34 157 PCT  
E--> 5138 - 48 -

*delete at end of file*

*PST*

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

## VERIFICATION SUMMARY

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Input Set : A:\PTO.txt

Output Set: C:\CRF3\05232001\I744016.raw

L:1 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:  
L:10 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:2464 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17  
L:2468 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17  
L:2472 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17  
L:2476 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17  
L:2480 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17  
L:2484 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17  
L:2488 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17  
L:2492 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17  
L:2496 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17  
L:2500 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17  
L:2504 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:17  
L:2928 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20  
L:2932 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20  
L:2936 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20  
L:2940 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20  
L:2944 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20  
L:2948 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20  
L:2952 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20  
L:2956 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20  
L:2960 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20  
L:2964 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20  
L:2968 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:20  
L:2972 M:254 E: No. of Bases conflict, LENGTH:Input:695 Counted:2291 SEQ:20  
L:3395 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:3398 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:3399 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:3402 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:3403 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:3406 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:3407 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:3410 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:3411 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:3415 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:3419 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:3422 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:3423 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:3427 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:3430 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23  
L:3431 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:3435 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:23  
L:3666 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:25  
M:340 Repeated in SeqNo=25  
L:3867 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:26  
L:3870 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:3871 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:26



## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/744,016

DATE: 05/23/2001

TIME: 12:31:19

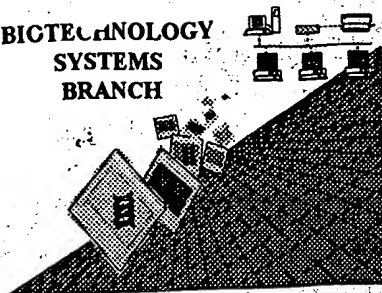
Input Set : A:\PTO.txt

Output Set: C:\CRF3\05232001\I744016.raw

L:3874 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:3875 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:26  
L:3878 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:3879 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:26  
L:3883 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:26  
L:3886 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:3887 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:26  
L:3891 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:26  
L:3894 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:3895 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:26  
L:3899 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:26  
L:3902 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:3903 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:26  
L:3906 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26  
L:3907 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:26  
L:4141 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28  
M:340 Repeated in SeqNo=28  
L:4330 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29  
L:4334 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29  
L:4338 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29  
L:4342 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29  
L:4346 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29  
L:4350 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:29  
L:5136 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:35  
L:5136 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:5136 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:2  
M:332 Repeated in SeqNo=35  
L:5138 M:252 E: No. of Seq. differs, <211>LENGTH:Input:19 Found:21 SEQ:35

## **RAW SEQUENCE LISTING** **ERROR REPORT**

BIO TECHNOLOGY  
SYSTEMS  
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

09/744,016

Source:

Pu/09

Date Processed by STIC:

5/23/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY.

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/744,016

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2        Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3        Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4        Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5        Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6        Variable Length      Sequence(s)        contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
- 7        PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s)       . Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223>  
sections for Artificial or Unknown sequences.
- 8        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      <210> sequence id number  
<400> sequence id number  
000
- 10        Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11        Use of "Artificial"      Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.  
(NEW RULES)      Valid response is Artificial Sequence.
- 12        Use of <220>Feature      Sequence(s)        are missing the <220>Feature and associated headings.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13        PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted  
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.